

## SEQUENCE LISTING

JAP20 Rec'd PCT/PTO 23 JUN 2006

&lt;110&gt; Kinch, Michael S.

&lt;120&gt; EphA2 VACCINES

&lt;130&gt; 10271-148

&lt;150&gt; US 60/532,696

&lt;151&gt; 2003-12-24

&lt;150&gt; US 60/602,588

&lt;151&gt; 2004-08-18

&lt;150&gt;

&lt;151&gt; 2004-10-01

&lt;150&gt;

&lt;151&gt; 2004-10-07

&lt;160&gt; 72

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 3963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (138)..(3068)

&lt;400&gt; 1

attaaggact cggggcagga ggggcagaag ttgcgcgcag gccggcgggc gggagcggac 60

accgaggccg gcgtgcaggc gtgcgggtgt gcgggagccg ggctcggggg gatcggaccg 120

agagcgcagaa gcgcggc atg gag ctc cag gca gcc cgc gcc tgc ttc gcc 170  
Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala  
1 5 10ctg ctg tgg ggc tgt gcg ctg gcc gcg gcc gcg gcg gcg cag ggc aag 218  
Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys  
15 20 25gaa gtg gta ctg ctg gac ttt gct gca gct gga ggg gag ctc ggc tgg 266  
Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp  
30 35 40ctc aca cac ccg tat ggc aaa ggg tgg gac ctg atg cag aac atc atg 314  
Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met  
45 50 55aat gac atg ccg atc tac atg tac tcc gtg tgc aac gtg atg tct ggc 362  
Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
60 65 70 75gac cag gac aac tgg ctc cgc acc aac tgg gtg tac cga gga gag gct 410  
Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala

-2-

cca cac tac ctc aca gcc gtg ggc atg ggt gcc aag gtg gag ctg cgc	1178
Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg	
335 340 345	
tgg acg ccc cct cag gac agc ggg ggc cgc gag gac att gtc tac agc	1226
Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser	
350 355 360	
gtc acc tgc gaa cag tgc tgg ccc gag tct ggg gaa tgc ggg ccg tgt	1274
Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys	
365 370 375	
gag gcc agt gtg cgc tac tcg gag cct cct cac gga ctg acc cgc acc	1322
Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr	
380 385 390 395	
agt gtg aca gtg agc gac ctg gag ccc cac atg aac tac acc ttc acc	1370
Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr	
400 405 410	
gtg gag gcc cgc aat ggc gtc tca ggc ctg gta acc agc cgc agc ttc	1418
Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe	
415 420 425	
cgt act gcc agt gtc agc atc aac cag aca gag ccc ccc aag gtg agg	1466
Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg	
430 435 440	
ctg gag ggc cgc agc acc acc tcg ctt agc gtc tcc tgg agc atc ccc	1514
Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro	
445 450 455	
ccg ccg cag cag agc cga gtg tgg aag tac gag gtc act tac cgc aag	1562
Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys	
460 465 470 475	
aag gga gac tcc aac agc tac aat gtg cgc cgc acc gag ggt ttc tcc	1610
Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser	
480 485 490	
gtg acc ctg gac gac ctg gcc cca gac acc acc tac ctg gtc cag gtg	1658
Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val	
495 500 505	
cag gca ctg acg cag gag ggc cag ggg gcc ggc agc aag gtg cac gaa	1706
Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu	
510 515 520	
ttc cag acg ctg tcc ccg gag gga tct ggc aac ttg gcg gtg att ggc	1754
Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly	
525 530 535	
ggc gtg gct gtc ggt gtg gtc ctg ctt ctg gtg ctg gca gga gtt ggc	1802
Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala Gly Val Gly	
540 545 550 555	
ttc ttt atc cac cgc agg agg aag aac cag cgt gcc cgc cag tcc ccg	1850
Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro	
560 565 570	

gag gac gtt tac ttc tcc aag tca gaa caa ctg aag ccc ctg aag aca	1898
Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr	
575 580 585	
tac gtg gac ccc cac aca tat gag gac ccc aac cag gct gtg ttg aag	1946
Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys	
590 595 600	
ttc act acc gag atc cat cca tcc tgt gtc act cgg cag aag gtg atc	1994
Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys Val Ile	
605 610 615	
gga gca gga gag ttt ggg gag gtg tac aag ggc atg ctg aag aca tcc	2042
Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser	
620 625 630 635	
tcg ggg aag aag gag gtg ccg gtg gcc atc aag acg ctg aaa gcc ggc	2090
Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly	
640 645 650	
tac aca gag aag cag cga gtg gac ttc ctc ggc gag gcc ggc atc atg	2138
Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met	
655 660 665	
ggc cag ttc agc cac cac aac atc atc cgc cta gag ggc gtc atc tcc	2186
Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser	
670 675 680	
aaa tac aag ccc atg atg atc atc act gag tac atg gag aat ggg gcc	2234
Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala	
685 690 695	
ctg gac aag ttc ctt cgg gag aag gat ggc gag ttc agc gtg ctg cag	2282
Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln	
700 705 710 715	
ctg gtg ggc atg ctg cgg ggc atc gca gct ggc atg aag tac ctg gcc	2330
Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala	
720 725 730	
aac atg aac tat gtg cac cgt gac ctg gct gcc cgc aac atc ctc gtc	2378
Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val	
735 740 745	
aac agc aac ctg gtc tgc aag gtg tct gac ttt ggc ctg tcc cgc gtg	2426
Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val	
750 755 760	
ctg gag gac gac ccc gag gcc acc tac acc acc agt ggc ggc aag atc	2474
Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile	
765 770 775	
ccc atc cgc tgg acc gcc ccg gag gcc att tcc tac cgg aag ttc acc	2522
Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr	
780 785 790 795	
tct gcc agc gac gtg tgg agc ttt ggc att gtc atg tgg gag gtg atg	2570
Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu Val Met	
800 805 810	
acc tat ggc gag cgg ccc tac tgg gag ttg tcc aac cac gag gtg atg	2618

Thr	Tyr	Gly	Glu	Arg	Pro	Tyr	Trp	Glu	Leu	Ser	Asn	His	Glu	Val	Met	
			815					820					825			
aaa	gcc	atc	aat	gat	ggc	ttc	cgg	ctc	ccc	aca	ccc	atg	gac	tgc	ccc	2666
Lys	Ala	Ile	Asn	Asp	Gly	Phe	Arg	Leu	Pro	Thr	Pro	Met	Asp	Cys	Pro	
		830					835				840					
tcc	gcc	atc	tac	cag	ctc	atg	atg	cag	tgc	tgg	cag	cag	gag	cgt	gcc	2714
Ser	Ala	Ile	Tyr	Gln	Leu	Met	Met	Gln	Cys	Trp	Gln	Gln	Glu	Arg	Ala	
	845				850						855					
cgc	cgc	ccc	aag	ttc	gct	gac	atc	gtc	agc	atc	ctg	gac	aag	ctc	att	2762
Arg	Arg	Pro	Lys	Phe	Ala	Asp	Ile	Val	Ser	Ile	Leu	Asp	Lys	Leu	Ile	
860				865					870					875		
cgt	gcc	cct	gac	tcc	ctc	aag	acc	ctg	gct	gac	ttt	gac	ccc	cgc	gtg	2810
Arg	Ala	Pro	Asp	Ser	Leu	Lys	Thr	Leu	Ala	Asp	Phe	Asp	Pro	Arg	Val	
			880					885						890		
tct	atc	cgg	ctc	ccc	agc	acg	agc	ggc	tcg	gag	ggg	gtg	ccc	ttc	cgc	2858
Ser	Ile	Arg	Leu	Pro	Ser	Thr	Ser	Gly	Ser	Glu	Gly	Val	Pro	Phe	Arg	
		895						900					905			
acg	gtg	tcc	gag	tgg	ctg	gag	tcc	atc	aag	atg	cag	cag	tat	acg	gag	2906
Thr	Val	Ser	Glu	Trp	Leu	Glu	Ser	Ile	Lys	Met	Gln	Gln	Tyr	Thr	Glu	
		910					915					920				
cac	ttc	atg	gcg	gcc	ggc	tac	act	gcc	atc	gag	aag	gtg	gtg	cag	atg	2954
His	Phe	Met	Ala	Ala	Gly	Tyr	Thr	Ala	Ile	Glu	Lys	Val	Val	Gln	Met	
	925					930					935					
acc	aac	gac	gac	atc	aag	agg	att	ggg	gtg	cgg	ctg	ccc	ggc	cac	cag	3002
Thr	Asn	Asp	Asp	Ile	Lys	Arg	Ile	Gly	Val	Arg	Leu	Pro	Gly	His	Gln	
940					945				950						955	
aag	cgc	atc	gcc	tac	agc	ctg	ctg	gga	ctc	aag	gac	cag	gtg	aac	act	3050
Lys	Arg	Ile	Ala	Tyr	Ser	Leu	Leu	Gly	Leu	Lys	Asp	Gln	Val	Asn	Thr	
			960					965						970		
gtg	ggg	atc	ccc	atc	tga	gcctcgacag	ggcctggagc	cccatcggcc								3098
Val	Gly	Ile	Pro	Ile												
		975														
aagaatactt	gaagaaacag	agtggcctcc	ctgctgtgcc	atgctgggcc	actggggact											3158
ttattttattt	ctagttcttt	cctccccctg	caacttccgc	tgaggggtct	cggatgacac											3218
cctggcctga	actgaggaga	tgaccagggga	tgctgggctg	ggcctctttt	cctgcgaga											3278
cgcacacagc	tgagcactta	gcaggcaccg	ccacgtccca	gcatccctgg	agcaggagcc											3338
ccgccacagc	cttcggacag	acatatagga	tattcccaag	ccgaccttcc	ctccgccttc											3398
tcccacatga	ggccatctca	ggagatggag	ggcttggccc	agcgccaagt	aaacagggta											3458
cctcaagccc	catttctctca	cactaagagg	gcagactgtg	aacttgactg	ggtgagaccc											3518
aaagcgggtcc	ctgtccctct	agtgccttct	ttagaccctc	gggccccatc	ctcatccctg											3578
actggccaaa	cccttgcttt	cctgggcctt	tgcaagatgc	ttggttgtgt	tgagggttttt											3638

```

aaatatatat tttgtacttt gtggagagaa tgtgtgtgtg tggcaggggg ccccgccagg 3698
gctgggggaca gaggggtgtca aacattcgtg agctgggggac tcagggaccg gtgctgcagg 3758
agtgtcctgc ccatgccccca gtcggccccca tctctcatcc ttttgataa gtttctattc 3818
tgtcagtgtt aaagattttg ttttgttgga catttttttc gaatcttaat ttattatttt 3878
ttttatattt attgtagaa aatgacttat ttctgctctg gaataaagtt gcagatgatt 3938
caaaccgaaa aaaaaaaaaa aaaaaa 3963

```

```

<210> 2
<211> 976
<212> PRT
<213> Homo sapiens

```

```

<400> 2

```

```

Met Glu Leu Gln Ala Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys
1          5          10          15

```

```

Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
          20          25          30

```

```

Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
          35          40          45

```

```

Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
          50          55          60

```

```

Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
65          70          75          80

```

```

Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile
          85          90          95

```

```

Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
          100          105          110

```

```

Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
          115          120          125

```

```

Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
          130          135          140

```

```

Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His
145          150          155          160

```

```

Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys

```

165										170					175				
Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp	Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu				
			180					185						190					
Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys	Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu				
		195					200					205							
Ala	His	Phe	Pro	Glu	Thr	Ile	Ala	Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala				
	210					215					220								
Thr	Val	Ala	Gly	Thr	Cys	Val	Asp	His	Ala	Val	Val	Pro	Pro	Gly	Gly				
225					230					235				240					
Glu	Glu	Pro	Arg	Met	His	Cys	Ala	Val	Asp	Gly	Glu	Trp	Leu	Val	Pro				
				245					250					255					
Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala	Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala				
		260						265					270						
Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe	Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser				
		275					280					285							
Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala				
	290					295					300								
Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro				
305					310					315				320					
Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro	Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr				
				325					330					335					
Ala	Val	Gly	Met	Gly	Ala	Lys	Val	Glu	Leu	Arg	Trp	Thr	Pro	Pro	Gln				
			340					345					350						
Asp	Ser	Gly	Gly	Arg	Glu	Asp	Ile	Val	Tyr	Ser	Val	Thr	Cys	Glu	Gln				
		355					360					365							
Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg				
	370					375					380								
Tyr	Ser	Glu	Pro	Pro	His	Gly	Leu	Thr	Arg	Thr	Ser	Val	Thr	Val	Ser				
385					390					395					400				
Asp	Leu	Glu	Pro	His	Met	Asn	Tyr	Thr	Phe	Thr	Val	Glu	Ala	Arg	Asn				
				405					410					415					

Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val  
 420 425 430

Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser  
 435 440 445

Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser  
 450 455 460

Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn  
 465 470 475 480

Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp  
 485 490 495

Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln  
 500 505 510

Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser  
 515 520 525

Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly  
 530 535 540

Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg  
 545 550 555 560

Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe  
 565 570 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His  
 580 585 590

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile  
 595 600 605

His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe  
 610 615 620

Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu  
 625 630 635 640

Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln  
 645 650 655



Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His  
660 665 670

His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met  
675 680 685

Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu  
690 695 700

Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu  
705 710 715 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val  
725 730 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val  
740 745 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro  
755 760 765

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr  
770 775 780

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val  
785 790 795 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg  
805 810 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp  
820 825 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
835 840 845

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe  
850 855 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser  
865 870 875 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro  
885 890 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp  
 900 905 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala  
 915 920 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile  
 930 935 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr  
 945 950 955 960

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 965 970 975

<210> 3  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 3

Thr Leu Ala Asp Phe Asp Pro Arg Val Pro Arg Thr  
 1 5 10

<210> 4  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Val Leu Leu Leu Val Leu Ala Gly Val  
 1 5

<210> 5  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Val Leu Ala Gly Val Gly Phe Phe Ile  
 1 5

<210> 6  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Ile Met Asn Asp Met Pro Ile Tyr Met  
1 5

<210> 7  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 7

Ser Leu Leu Gly Leu Lys Asp Gln Val  
1 5

<210> 8  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 8

Trp Leu Val Pro Ile Gly Gln Cys Leu  
1 5

<210> 9  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 9

Leu Leu Trp Gly Cys Ala Leu Ala Ala  
1 5

<210> 10  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 10

Gly Leu Thr Arg Thr Ser Val Thr Val  
1 5

<210> 11  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 11

Asn Leu Tyr Tyr Ala Glu Ser Asp Leu  
1 5

<210> 12

<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 12

Lys Leu Asn Val Glu Glu Arg Ser Val  
1 5

<210> 13  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 13

Ile Met Gly Gln Phe Ser His His Asn  
1 5

<210> 14  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 14

Tyr Ser Val Cys Asn Val Met Ser Gly  
1 5

<210> 15  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 15

Met Gln Asn Ile Met Asn Asp Met Pro  
1 5

<210> 16  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 16

Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg  
1 5 10 15

<210> 17  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 17

Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
 1 5 10

<210> 18  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser  
 1 5 10 15

<210> 19  
 <211> 3105  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct

<400> 19  
 atgaaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60  
 caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120  
 ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180  
 gagctccagg cagccccgcg ctgcttcgcc ctgctgtggg gctgtgcgct ggccgcggcc 240  
 gcggcgggcg agggcaagga agtggtactg ctggactttg ctgcagctgg aggggagctc 300  
 ggctggctca cacacccgta tggcaaaggg tgggacctga tgcagaacat catgaatgac 360  
 atgccgatct acatgtactc cgtgtgcaac gtgatgtctg gcgaccagga caactggctc 420  
 cgcaccaact ggggtgtacc aggagaggct gagcgatatct tcattgagct caagtttact 480  
 gtacgtgact gcaacagctt ccctgggtgg gccagctcct gcaaggagac tttcaacctc 540  
 tactatgccg agtcggacct ggactacggc accaacttcc agaagcgcct gttcaccaag 600  
 attgacacca ttgcgcccga tgagatcacc gtcagcagcg acttcgaggc acgccacgtg 660  
 aagctgaacg tggaggagcg ctccgtgggg ccgctcaccc gcaaaggctt ctacctggcc 720  
 ttccaggata tccgtgctg tgtggcgctg ctctccgtcc gtgtctacta caagaagtgc 780  
 cccgagctgc tgcagggcct ggcccacttc cctgagacca tcgccggctc tgatgcacct 840  
 tccctggcca ctgtggccgg cacctgtgtg gaccatgccg tgggtgccacc ggggggtgaa 900  
 gagccccgta tgcactgtgc agtggatggc gagtggctgg tgcccattgg gcagtgcctg 960  
 tgccaggcag gctacgagaa ggtggaggat gcctgccagg cctgctcgcc tggatttttt 1020  
 aagtttgagg catctgagag ccctgcttg gagtgcctg agcacacgct gccatcccct 1080

gaggggtgcc	cctcctgcga	gtgtgaggaa	ggcttcttcc	gggcacctca	ggacccagcg	1140
tcgatgcctt	gcacacgacc	cccctccgcc	ccacactacc	tcacagccgt	gggcatgggt	1200
gccaaggtgg	agctgcgctg	gacgccccct	caggacagcg	ggggccgcga	ggacattgtc	1260
tacagcgtea	cctgcgaaca	gtgctggccc	gagtctgggg	aatgcggggc	gtgtgaggcc	1320
agtgtgcgct	actcggagcc	tcctcacgga	ctgaccgcga	ccagtgtgac	agtgagcgac	1380
ctggagcccc	acatgaacta	caccttcacc	gtggaggccc	gcaatggcgt	ctcaggcctg	1440
gtaaccagcc	gcagcttccg	tactgccagt	gtcagcatca	accagacaga	gcccccaag	1500
gtgaggctgg	agggccgcag	caccacctcg	cttagcgtct	cctggagcat	ccccccgccg	1560
cagcagagcc	gagtgtggaa	gtacgaggtc	acttaccgca	agaagggaga	ctccaacagc	1620
tacaatgtgc	gccgcaccga	gggtttctcc	gtgaccctgg	acgacctggc	cccagacacc	1680
acctacctgg	tccaggtgca	ggcactgacg	caggagggcc	agggggccgg	cagcaggggtg	1740
cacgaattcc	agacgctgtc	cccggagggg	tctggcaact	tggcgggtgat	tggcggcgtg	1800
gctgtcgggtg	tggtcctgct	tctggtgctg	gcaggagttg	gcttctttat	ccaccgcagg	1860
aggaagaacc	agcgtgcccc	ccagtccccg	gaggacgttt	acttctccaa	gtcagaacaa	1920
ctgaagcccc	tgaagacata	cgtggacccc	cacacatatg	aggaccccaa	ccaggctgtg	1980
ttgaagttca	ctaccgagat	ccatccatcc	tgtgtcactc	ggcagaaggt	gatcggagca	2040
ggagagtttg	gggaggtgta	caagggcatg	ctgaagacat	cctcggggaa	gaaggaggtg	2100
ccggtggcca	tcaagacgct	gaaagccggc	tacacagaga	agcagcgagt	ggacttcctc	2160
ggcgaggccg	gcatcatggg	ccagttcagc	caccacaaca	tcatccgcct	agagggcgctc	2220
atctccaaat	acaagcccat	gatgatcatc	actgagtaca	tggagaatgg	ggccctggac	2280
aagtctcttc	gggagaagga	tggcgagttc	agcgtgctgc	agctggtggg	catgctgcgg	2340
ggcatcgag	ctggcatgaa	gtacctggcc	aacatgaact	atgtgcaccg	tgacctggct	2400
gcccgaaca	tcctcgtaaa	cagcaacctg	gtctgcaagg	tgtctgactt	tggcctgtcc	2460
cgctgtctgg	aggacgaccc	cgaggccacc	tacaccacca	gtggcgga	gatccccatc	2520
cgctggaccg	ccccggaggc	catttcctac	cggaagttca	cctctgccag	cgacgtgtgg	2580
agctttggca	ttgtcatgtg	ggagggtgatg	acctatggcg	agcggcccta	ctgggagttg	2640
tccaaccacg	aggtgatgaa	agccatcaat	gatggcttcc	ggctccccac	acccatggac	2700
tgccccctcg	ccatctacca	gctcatgatg	cagtgtctggc	agcaggagcg	tgccccccgc	2760
cccaagttcg	ctgacatcgt	cagcatcctg	gacaagctca	tctgtgcccc	tgactccctc	2820
aagaccctgg	ctgactttga	ccccgcgtg	tctatccggc	tccccagcac	gagcggctcg	2880
gaggggggtgc	ccttccgcac	ggtgtccgag	tggctggagt	ccatcaagat	gcagcagtat	2940

acggagcact tcattggcggc cggctacact gccatcgaga aggtggtgca gatgaccaac 3000  
gacgacatca agaggattgg ggtgcggctg cccggccacc agaagcgcat cgcctacagc 3060  
ctgctgggac tcaaggacca ggtgaacact gtggggatcc ccatc 3105

<210> 20

<211> 1035

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 20

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Leu Gln Ala  
50 55 60

Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala  
65 70 75 80

Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala  
85 90 95

Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp  
100 105 110

Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val  
115 120 125

Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp  
130 135 140

Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr  
145 150 155 160

Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu  
165 170 175

Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn  
 180 185 190

Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu  
 195 200 205

Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val  
 210 215 220

Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala  
 225 230 235 240

Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr  
 245 250 255

Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu  
 260 265 270

Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr  
 275 280 285

Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met  
 290 295 300

His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu  
 305 310 315 320

Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser  
 325 330 335

Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys  
 340 345 350

Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys  
 355 360 365

Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys  
 370 375 380

Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly  
 385 390 395 400

Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg  
 405 410 415



Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser  
 420 425 430

Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro  
 435 440 445

His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His  
 450 455 460

Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu  
 465 470 475 480

Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr  
 485 490 495

Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser  
 500 505 510

Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr  
 515 520 525

Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg  
 530 535 540

Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr  
 545 550 555 560

Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala  
 565 570 575

Gly Ser Arg Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly  
 580 585 590

Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu  
 595 600 605

Val Leu Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln  
 610 615 620

Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln  
 625 630 635 640

Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro  
 645 650 655

Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val  
 660 665 670

Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys  
 675 680 685

Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile  
 690 695 700

Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu  
 705 710 715 720

Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg  
 725 730 735

Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu  
 740 745 750

Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly  
 755 760 765

Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala  
 770 775 780

Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala  
 785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp  
 805 810 815

Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr  
 820 825 830

Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile  
 835 840 845

Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile  
 850 855 860

Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu  
 865 870 875 880

Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro  
 885 890 895

Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys

	900		905		910										
Trp	Gln	Gln	Glu	Arg	Ala	Arg	Arg	Pro	Lys	Phe	Ala	Asp	Ile	Val	Ser
	915						920					925			
Ile	Leu	Asp	Lys	Leu	Ile	Arg	Ala	Pro	Asp	Ser	Leu	Lys	Thr	Leu	Ala
	930					935					940				
Asp	Phe	Asp	Pro	Arg	Val	Ser	Ile	Arg	Leu	Pro	Ser	Thr	Ser	Gly	Ser
945					950					955					960
Glu	Gly	Val	Pro	Phe	Arg	Thr	Val	Ser	Glu	Trp	Leu	Glu	Ser	Ile	Lys
				965					970					975	
Met	Gln	Gln	Tyr	Thr	Glu	His	Phe	Met	Ala	Ala	Gly	Tyr	Thr	Ala	Ile
			980					985					990		
Glu	Lys	Val	Val	Gln	Met	Thr	Asn	Asp	Asp	Ile	Lys	Arg	Ile	Gly	Val
	995						1000					1005			
Arg	Leu	Pro	Gly	His	Gln	Lys	Arg	Ile	Ala	Tyr	Ser	Leu	Leu	Gly	
	1010					1015					1020				
Leu	Lys	Asp	Gln	Val	Asn	Thr	Val	Gly	Ile	Pro	Ile				
	1025					1030					1035				

&lt;210&gt; 21

&lt;211&gt; 1506

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

cagggcaagg aagtgtact gctggacttt gctgcagctg gaggggagct cggctggctc	60
acacacccgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgac	120
tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct ccgcaccaac	180
tggtgtacc gaggagaggc tgagcgtatc ttcatgagc tcaagtttac tgtacgtgac	240
tgcaacagct tccctggtgg cgccagctcc tgcaaggaga ctttcaacct ctactatgcc	300
gagtcggacc tggactacgg caccaacttc cagaagcgcc tgttcaccaa gattgacacc	360
attgcgccc atgagatcac cgtcagcagc gacttcgagg cagccacgt gaagctgaac	420
gtggaggagc gctccgtggg gccgctcacc cgcaaaggct tctacctggc cttccaggat	480
atcggtgct gtgtggcgct gctctccgtc cgtgtctact acaagaagtg ccccgagctg	540
ctgcagggcc tggcccactt ccctgagacc atcgccggct ctgatgcacc ttccctggcc	600

```

actgtggccg gcacctgtgt ggaccatgcc gtggtgccac cgggggggtga agagccccgt    660
atgcactgtg cagtggatgg cgagtggctg gtgcccattg ggcagtgcct gtgccaggca    720
ggctacgaga aggtggagga tgcctgccag gcctgctcgc ctggattttt taagtttgag    780
gcatctgaga gcccctgctt ggagtgccct gagcacacgc tgccatcccc tgaggggtgcc    840
acctcctgcg agtgtgagga aggtttcttc cggggcacctc aggaccacgc gtcgatgcct    900
tgcacacgac ccccctccgc cccacactac ctcacagccg tgggcatggg tgccaagggtg    960
gagctgcgct ggacgcccc ctaggacagc gggggccgcg aggacattgt ctacagcgtc   1020
acctgcgaac agtgcctggc cgagtctggg gaatgcgggc cgtgtgaggc cagtgtgcgc   1080
tactcggagc ctcttcacgg actgaccgc accagtgtga cagtgagcga cctggagccc   1140
cacatgaact acaccttcac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc   1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agcccccaa ggtgaggctg   1260
gagggccgca gcaccacctc gcttagcgtc tcttgagcga tccccccgcc gcagcagagc   1320
cgagtgtgga agtacgaggt cacttacgc aagaaggag actccaacag ctacaatgtg   1380
cgccgcaccg agggtttctc cgtgaccctg gacgacctgg cccagacac cacctacctg   1440
gtccaggtgc aggcactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc   1500
cagacg                                           1506

```

&lt;210&gt; 22

&lt;211&gt; 1506

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Human sequence optimized for codon usage in Listeria

&lt;400&gt; 22

```

caaggtaaag aagttgtttt attagatttt gcagcagcag gtggtgaatt aggttggtta    60
acacatccat atggtaaagg ttgggattta atgcaaaata ttatgaatga tatgccaat    120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattggtt acgtacaaat    180
tgggtttatc gtggtgaagc agaacgtatt ttatttgaat taaaatttac agttcgtgat    240
tgtaatatgt ttccagggtg tgcaagtagt tgtaaagaaa catttaattt atattatgca    300
gaaagtgatt tagattatgg tacaaatttt caaaaacgtt tatttacaaa aattgataca    360
attgcaccag atgaaattac agttagtagt gattttgaag cacgtcatgt taaattaaat    420
gttgaagaac gtagtgttgg tccattaaca cgtaaagggt ttatttttagc atttcaagat    480
attggtgcat gtgttgcat attaagtgtt cgtgtttatt ataaaaaatg tccagaatta    540

```

ttacaagggt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca 600  
 acagttgcag gtacatgtgt tgatcatgca gttgttccac caggtggtga agaaccacgt 660  
 atgcattgtg cagttgatgg tgaatgggta gttccaattg gtcaatgttt atgtcaagca 720  
 gggttatgaaa aagttgaaga tgcattgtcaa gcatgtagtc cagggtttttt taaatttgaa 780  
 gcaagtgaaa gtccatgttt agaattgtcca gaacatacat taccaagtcc agaagggtgca 840  
 acaagttgtg aatgtgaaga aggttttttt cgtgcaccac aagatccagc aagtatgcca 900  
 tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt 960  
 gaattacgtt ggacaccacc acaagatagt ggtggtcgtg aagatattgt ttatagtgtt 1020  
 acatgtgaac aatgttggcc agaaagtggg gaatgtggtc catgtgaagc aagtgttcgt 1080  
 tatagtgaac caccacatgg tttaacacgt acaagtgtta cagttagtga tttagaacca 1140  
 catatgaatt atacatttac agttgaagca cgtaatgggt ttagtgggtt agttacaagt 1200  
 cgtagttttc gtacagcaag tgtagtatt aatcaaacag aaccaccaa agttcgttta 1260  
 gaaggtcgta gtacaacaag tttaagtgtt agttggagta ttccaccacc acaacaaagt 1320  
 cgtgtttgga aatatgaagt tacatatcgt aaaaaagggt atagtaatag ttataatgtt 1380  
 cgtcgtacag aagggttttag tgttacatta gatgatttag caccagatac aacatattta 1440  
 gttcaagttc aagcattaac acaagaaggt caagggtgcag gtagtcgtgt tcatgaattt 1500  
 caaaca 1506

<210> 23  
 <211> 502  
 <212> PRT  
 <213> Homo sapeins

<400> 23

Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu  
 1 5 10 15

Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln  
 20 25 30

Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val  
 35 40 45

Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg  
 50 55 60

Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp

65	70	75	80
Cys Asn Ser Phe	Pro Gly Gly Ala Ser	Ser Cys Lys Glu Thr	Phe Asn
	85	90	95
Leu Tyr Tyr Ala	Glu Ser Asp Leu Asp Tyr Gly Thr Asn	Phe Gln Lys	
	100	105	110
Arg Leu Phe Thr	Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val		
	115	120	125
Ser Ser Asp Phe	Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg		
	130	135	140
Ser Val Gly Pro	Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp		
	145	150	155
Ile Gly Ala Cys	Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys		
	165	170	175
Cys Pro Glu Leu	Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala		
	180	185	190
Gly Ser Asp Ala	Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp		
	195	200	205
His Ala Val Val	Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala		
	210	215	220
Val Asp Gly Glu	Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala		
	225	230	235
Gly Tyr Glu Lys	Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe		
	245	250	255
Phe Lys Phe Glu	Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His		
	260	265	270
Thr Leu Pro Ser	Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly		
	275	280	285
Phe Phe Arg Ala	Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro		
	290	295	300
Pro Ser Ala Pro	His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val		
	305	310	315
			320

-23-

```

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
gagcagggca aggaagtggc actgctggac tttgctgcag ctggagggga gctcggctgg 240
ctcacacacc cgtatggcaa aggggtggac ctgatgcaga acatcatgaa tgacatgccg 300
atctacatgt actccgtgtg caacgtgatg tctggcgacc aggacaactg gctccgcacc 360
aactgggtgt accgaggaga ggctgagcgt atcttcattg agctcaagtt tactgtacgt 420
gactgcaaca gcttcacctg tggcgccagc tctgcaagg agactttcaa cctctactat 480
gccgagtcgg acctggacta cggcaccaac ttccagaagc gcctgttcac caagattgac 540
accattgcgc ccgatgagat caccgtcagc agcgacttcg aggcacgcca cgtgaagctg 600
aacgtggagg agcgctccgt ggggcccgtc acccgcaaag gcttctacct ggccctccag 660
gatatcggtg cctgtgtggc gctgctctcc gtccgtgtct actacaagaa gtgccccgag 720
ctgctgcagg gcctggccca cttccctgag accatcgccg gctctgatgc accttcctg 780
gccactgtgg ccggcacctg tgtggaccat gccgtggtgc caccgggggg tgaagagccc 840
cgtatgcact gtgcagtgga tggcgagtgg ctggtgcccc ttgggcagtg cctgtgccag 900
gcaggctacg agaaggtgga ggatgcctgc caggcctgct cgcttgatt ttttaagttt 960
gaggcatctg agagcccctg cttggagtgc cctgagcaca cgctgccatc ccctgagggg 1020
gccacctcct gcgagtgtga ggaaggcttc ttccgggcac ctcaggaccc agcgtcgatg 1080
ccttgcacac gacccccctc cgccccacac tacctcacag ccgtgggcat gggtgccaag 1140
gtggagctgc gctggacgcc ccctcaggac agcgggggcc gcgaggacat tgtctacagc 1200
gtcacctgcg aacagtgcct gcccgagtct ggggaatgcg ggccgtgtga ggccagtgtg 1260
cgctactcgg agcctcctca cggactgacc cgcaccagtg tgacagtgag cgacctggag 1320
ccccacatga actacacctt caccgtggag gcccgcaatg gcgtctcagg cctggtaacc 1380
agccgcagct tccgtactgc cagtgtcagc atcaaccaga cagagcccc caaggtgagg 1440
ctggagggcc gcagcaccac ctcgcttagc gtctcctgga gcatcccccc gccgcagcag 1500
agccgagtgt ggaagtacga ggtcacttac cgcaagaagg gagactcaa cagctacaat 1560
gtgcgccgca ccgaggggtt ctccgtgacc ctggacgacc tggccccaga caccacctac 1620
ctggtccagg tgcaggcact gacgcaggag ggccaggggg ccggcagcag ggtgcacgaa 1680
ttccagacg 1689

```

&lt;210&gt; 25

&lt;211&gt; 563

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 25

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Gln Gly Lys  
 50 55 60

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp  
 65 70 75 80

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met  
 85 90 95

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly  
 100 105 110

Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala  
 115 120 125

Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser  
 130 135 140

Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr  
 145 150 155 160

Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe  
 165 170 175

Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp  
 180 185 190

Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly  
 195 200 205

Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala  
 210 215 220

Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu  
225 230 235 240

Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp  
245 250 255

Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val  
260 265 270

Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly  
275 280 285

Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu  
290 295 300

Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe  
305 310 315 320

Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro  
325 330 335

Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg  
340 345 350

Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala  
355 360 365

Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg  
370 375 380

Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser  
385 390 395 400

Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys  
405 410 415

Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr  
420 425 430

Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr  
435 440 445

Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe  
450 455 460

Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg  
465 470 475 480

Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro  
485 490 495

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys  
500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser  
515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val  
530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu  
545 550 555 560

Phe Gln Thr

<210> 26

<211> 1989

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein construct

<400> 26

```

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac      60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata      120
at attgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg      180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg      240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa      300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcac catggcacca      360
ccagcatctc cgcttgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc      420
gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca      480

gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttggga tttaatgcaa      540
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtgggtgat      600
caagataatt ggttacgtac aaattgggtt tatcgtggtg aagcagaacg tatttttatt      660

```

```

gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900
ggtttttatt tagcatttca agatattggt gcatgtgttg cattattaag tgttcgtgtt 960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca 1020
ggtagtgatg caccaagttt agcaacagtt gcaggtagat gtgttgatca tgcagttgtt 1080
ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca 1140
attggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt 1200
agtccagggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtgg 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tggatgaatgt 1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
ggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaagttcg tttagaaggc cgtagtacaa caagtttaag tgtaggtgg 1740
agtattccac caccacaaca aagtcgtgtt tggaaatatg aagttacata tcgtaaaaaa 1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtggtac attagatgat 1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagg 1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta 1980
tgagagctc 1989

```

<210> 27

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 27

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala  
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly  
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr  
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr  
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys  
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys  
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly  
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro  
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu  
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr  
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg  
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe  
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala  
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro  
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln  
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala  
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu  
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys  
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met  
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly  
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly  
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro  
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu  
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu  
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser  
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn  
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser  
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp

	500		505		510
Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn					
	515		520		525
Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro					
	530		535		540
Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln					
	545		550		555
Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile					
		565		570	575
Ser Glu Glu Asp Leu					
	580				

<210> 28  
 <211> 1989  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct for fusion protein

<400> 28  
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcgtt tcattctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 aaaaaaatta tgtagtttt tattacatta attttagtta gttaccaat tgcacaacaa 300  
 acagaagcaa aagatgcaag tgcatttaaat aaagaaaata gtattagtag tatggcacca 360  
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420  
 gattataaag atgatgatga taaacaagggt aaagaagttg ttttattaga ttttgcagca 480  
 gcaggtggtg aattaggttg gttaacacat ccatatggta aagggtggga tttaatgcaa 540  
 aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtgggtgat 600  
 caagataatt gggtacgtac aaattgggtt tatcgtggtg aagcagaacg tatttttatt 660  
 gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720  
 gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780  
 cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840  
 gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900

```

ggtttttatt tagcatttca agatattggt gcatgtgttg cattattaag tgttcgtggt      960
tattataaaa aatgtccaga attattacaa ggttttagcac attttccaga aacaattgca      1020
ggtagtgatg caccaagttt agcaacagtt gcaggtacat gtgttgatca tgcagttggt      1080
ccaccaggtg gtgaagaacc acgtatgcat tgtgcagttg atgggtgaatg gttagttcca      1140
attgggtcaat gtttatgtca agcagggttat gaaaaagttg aagatgcatg tcaagcatgt      1200
agtccaggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat      1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca      1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca      1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtgggtggt      1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt      1500
gggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atgggtttaac acgtacaagt      1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat      1620
gggtgtagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa      1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgtaggttgg      1740
agtattccac caccacaaca aagtcgtggt tggaaatatg aagttacata tcgtaaaaaa      1800
ggtgatagta atagttataa tggtcgtcgt acagaaggtt ttagtggtac attagatgat      1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaaggt      1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta      1980
tgagagctc

```

<210> 29  
 <211> 581  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Predicted Fusion protein

<400> 29

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20          25          30

```

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35          40          45

```



Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala  
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly  
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr  
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr  
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys  
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys  
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly  
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro  
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu  
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr  
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg  
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe  
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala  
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro  
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln  
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala  
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu  
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys  
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met  
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly  
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly  
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro  
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu  
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu  
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser  
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn  
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser  
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp  
 500 505 510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn  
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro  
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln  
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile  
 565 570 575

Ser Glu Glu Asp Leu  
 580

<210> 30  
 <211> 1968  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 30  
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcggtt tcattctttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300  
 aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360  
 ggattaacga ttgccagtc gggtggggcc tttggatccg attataaaga tgatgatgat 420  
 aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggtga attaggttgg 480  
 ttaacacatc catatggtaa aggttgggat ttaatgcaa atattatgaa tgatatgcca 540  
 atttatatgt atagtgtttg taatgttatg agtggtgatc aagataattg gttacgtaca 600  
 aattgggttt atcgtggtga agcagaacgt atttttattg aattaaaatt tacagttcgt 660  
 gattgtaata gttttccagg tgggtgcaagt agttgtaaag aaacatttaa tttatattat 720  
 gcagaaagtg atttagatta tgggtacaaat tttcaaaaac gtttatttac aaaaattgat 780  
 acaattgcac cagatgaaat tacagttagt agtgattttg aagcacgtca tgttaaatta 840  
 aatggtgaag aacgtagtgt tgggtccatta acacgtaaag gtttttattt agcatttcaa 900  
 gatattggtg catgtgttgc attattaagt gttcgtgttt attataaaaa atgtccagaa 960  
 ttattacaag gtttagcaca ttttccagaa acaattgcag gtagtgatgc accaagttta 1020  
 gcaacagttg caggtacatg tgttgatcat gcagttgttc caccaggtgg tgaagaacca 1080

```

cgtatgcatt gtgcagttga tggatgaatgg ttagttccaa ttggtcaatg tttatgtcaa 1140
gcaggttatg aaaaagttga agatgcatgt caagcatgta gtccagggtt ttttaaattt 1200
gaagcaagtg aaagtccatg tttagaatgt ccagaacata cattaccaag tccagaaggt 1260
gcaacaagtt gtgaatgtga agaagggttt tttcgtgcac cacaagatcc agcaagtatg 1320
ccatgtacac gtccaccaag tgcaccacat tatttaacag cagttggtat ggggtcaaaa 1380
gttgaattac gttggacacc accacaagat agtggtggtc gtgaagatat tgtttatagt 1440
gttacatgtg aacaatgttg gccagaaagt ggtgaatgtg gtccatgtga agcaagtgtt 1500
cgttatagtg aaccaccaca tggtttaaca cgtacaagtg ttacagttag tgatttagaa 1560
ccacatatga attatacatt tacagttgaa gcacgtaatg gtgttagtgg tttagttaca 1620
agtcgtagtt ttcgtacagc aagtgttagt attaatacaa cagaaccacc aaaagttcgt 1680
ttagaagggtc gtagtacaac aagtttaagt gttagttgga gtattccacc accacaacaa 1740
agtcgtgttt ggaaatatga agttacatat cgtaaaaaag gtgatagtaa tagttataat 1800
gttcgtcgta cagaagggtt tagtgttaca ttagatgatt tagcaccaga tacaacatat 1860
ttagttcaag ttcaagcatt aacacaagaa ggtcaagggtg caggtagtcg tgttcatgaa 1920
tttcaaacag aacaaaaaatt aattagttaa gaagatttat gagagctc 1968

```

&lt;210&gt; 31

&lt;211&gt; 574

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted Fusion Protein

&lt;400&gt; 31

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10          15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
          20          25          30

```

```

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
          35          40          45

```

```

Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gln Gly
          50          55          60

```

```

Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly
        65          70          75          80

```

Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile  
85 90 95

Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser  
100 105 110

Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu  
115 120 125

Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn  
130 135 140

Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr  
145 150 155 160

Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu  
165 170 175

Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser  
180 185 190

Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val  
195 200 205

Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly  
210 215 220

Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro  
225 230 235 240

Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser  
245 250 255

Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala  
260 265 270

Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp  
275 280 285

Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr  
290 295 300

Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys  
305 310 315 320

Glu Phe Gln Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

565

570

<210> 32  
 <211> 1254  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 caccgcagga ggaagaacca gcgtgcccgc cagtccccgc aggacgttta cttctccaag 60  
 tcagaacaac tgaagcccct gaagacatac gtggaccccc acacatatga ggaccccaac 120  
 caggctgtgt tgaagtccac taccgagatc catccatcct gtgtcactcg gcagaagggtg 180  
 atcggagcag gagagtttgg ggaggtgtac aagggcatgc tgaagacatc ctcggggaag 240  
 aaggaggtgc cgggtggccat caagacgctg aaagccggct acacagagaa gcagcgagtgc 300  
 gacttcctcg gcgaggccgc catcatgggc cagttcagcc accacaacat catccgccta 360  
 gaggggcgtca tctccaaata caagcccatg atgatcatca ctgagtacat ggagaatggg 420  
 gccctggaca agttccttcg ggagaaggat ggcgagttca gcgtgctgca gctggtgggc 480  
 atgctgcggg gcatcgcagc tggcatgaag tacctggcca acatgaacta tgtgcaccgt 540  
 gacctggctg cccgcaacat cctcgtcaac agcaacctgg tctgcaaggt gtctgacttt 600  
 ggctgtccc gcgtgctgga ggacgacccc gagggcacct acaccaccag tggcggcaag 660  
 atcccatcc gctggaccgc cccggaggcc atttccctacc ggaagttcac ctctgccagc 720  
 gacgtgtgga gctttggcat tgtcatgtgg gaggtgatga cctatggcga gcggccctac 780  
 tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttcctg gctccccaca 840  
 cccatggact gccctccgc catctaccag ctcatgatgc agtgctggca gcaggagcgt 900  
 gcccgccgc ccaagttcgc tgacatcgtc agcatcctgg acaagctcat tcgtgcccct 960  
 gactccctca agaccctggc tgactttgac ccccgctgt ctatccggct cccagcacg 1020  
 agcggctcgg aggggggtgc cttccgcacg gtgtccgagt ggctggagtc catcaagatg 1080  
 cagcagtata cggagcactt catggcggcc ggctacactg ccatcgagaa ggtggtgcag 1140  
 atgaccaacg acgacatcaa gaggattggg gtgcggctgc ccggccacca gaagcgcac 1200  
 gcctacagcc tgctgggact caaggaccag gtgaacactg tggggatccc catc 1254

<210> 33  
 <211> 1254  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

<400> 33  
cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta tttttcgaaa 60  
agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaaat 120  
caagcagtat taaaatttac aacagaaata caccgaagtt gtgttacaag acaaaaagtt 180  
attggagcag gtgaattcgg agaggtatat aaaggtatgt taaaaacatc atcaggtaaa 240  
aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt 300  
gatttttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg 360  
gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat ggaaaacggt 420  
gcttttagata aattttttacg tgaaaaggat ggtgaattta gtgttttaca attggttggt 480  
atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt 540  
gatttggcag caagaaatat cctagtcaat tccaatttag tatgtaaagt tagtgatttt 600  
ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa 660  
attcctattc gttggacagc accagaagct atcagttacc gtaaatttac aagtgcacat 720  
gacgtgtgga gttttgggat tgtaatgtgg gaagttatga catatggaga aagaccatat 780  
tgggaaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact 840  
ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatggtggca acaagaaaga 900  
gcacgacgtc caaaatttgc agatattgtt agtatttttag acaaattaat tcgtgcacca 960  
gatagtttaa aaacttttagc agactttgat cctcgtgtta gtattcgatt accaagtacg 1020  
tcagggttccg aaggagttcc atttcgcaca gtctccgaat gggttgaatc aattaaatg 1080  
caacaatata ccgaacactt tatggcagca gggtacacag caatcgaaaa agttgttcaa 1140  
atgacaaatg atgatattaa acgtattgga gttagattac caggccacca gaaacgtatt 1200  
gcatattctt tattagggtt aaaagatcaa gttaataccg tgggaattcc aatt 1254

<210> 34  
<211> 456  
<212> PRT  
<213> Homo sapiens

<400> 34

Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala  
1 5 10 15

Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala  
20 25 30

Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg  
35 40 45



Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro  
 50 55 60

Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala  
 65 70 75 80

Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln  
 85 90 95

Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu  
 100 105 110

Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu  
 115 120 125

Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala  
 130 135 140

Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly  
 145 150 155 160

Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu  
 165 170 175

Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser  
 180 185 190

Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys  
 195 200 205

Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn  
 210 215 220

Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu  
 225 230 235 240

Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly  
 245 250 255

Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg  
 260 265 270

Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp  
 275 280 285

Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His  
 290 295 300

Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met  
 305 310 315 320

Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln  
 325 330 335

Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp  
 340 345 350

Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp  
 355 360 365

Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val  
 370 375 380

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln  
 385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val  
 405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro  
 420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln  
 435 440 445

Val Asn Thr Val Gly Ile Pro Ile  
 450 455

<210> 35

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein

<400> 35

atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120

ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180

gagcaccgca ggaggaagaa ccagcgtgcc cgccagtccc cggaggacgt ttactttctcc 240  
 aagtcagaac aactgaagcc cctgaagaca tacgtggacc cccacacata tgaggacccc 300  
 aaccaggctg tgttgaagtt cactaccgag atccatccat cctgtgtcac tcggcagaag 360  
 gtgatcggag caggagagtt tggggaggtg tacaagggca tgctgaagac atcctcgggg 420  
 aagaaggagg tgccggtggc catcaagacg ctgaaagccg gctacacaga gaagcagcga 480  
 gtggacttcc tcggcgaggc cggcatcatg ggccagttca gccaccacaa catcatccgc 540  
 ctagagggcg tcattctcaa atacaagccc atgatgatca tcaactgagta catggagaat 600  
 ggggccctgg acaagttcct tcgggagaag gatggcgagt tcagcgtgct gcagctggtg 660  
 ggcattgctgc ggggcattgc agctggcatg aagtacctgg ccaacatgaa ctatgtgcac 720  
 cgtgacctgg ctgcccgcaa catcctcgtc aacagcaacc tggctctgaa ggtgtctgac 780  
 tttggcctgt cccgctgct ggaggacgac cccgaggcca cctacaccac cagtggcggc 840  
  
 aagatcccca tccgctggac cgccccggag gccatttctt accggaagtt cacctctgcc 900  
 agcgacgtgt ggagctttgg cattgtcatg tgggaggtga tgacctatgg cgagcggccc 960  
 tactgggagt tgtccaacca cgaggtgatg aaagccatca atgatggctt ccggctcccc 1020  
 acacccatgg actgcccctc cgccatctac cagctcatga tgcagtgtg gcagcaggag 1080  
 cgtgcccgc gccccaagtt cgctgacatc gtcagcatcc tggacaagct cattcgtgcc 1140  
 cctgactccc tcaagaccct ggctgacttt gacccccgcg tgtctatccg gctccccagc 1200  
 acgagcggct cggagggggg gcccttcgc acggtgtccg agtggctgga gtccatcaag 1260  
 atgcagcagt atacggagca cttcatggcg gccggctaca ctgccatcga gaaggtggtg 1320  
 cagatgacca acgacgacat caagaggatt ggggtgcggc tgcccggcca ccagaagcgc 1380  
 atcgctaca gcctgctggg actcaaggac caggtgaaca ctgtggggat ccccatc 1437

&lt;210&gt; 36

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted Protein Sequence

&lt;400&gt; 36

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu His Arg Arg  
 50 55 60

Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser  
 65 70 75 80

Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr  
 85 90 95

Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His  
 100 105 110

Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly  
 115 120 125

Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val  
 130 135 140

Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg  
 145 150 155 160

Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His  
 165 170 175

Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met  
 180 185 190

Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg  
 195 200 205

Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg  
 210 215 220

Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His  
 225 230 235 240

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys  
 245 250 255

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu  
 260 265 270

Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala  
 275 280 285

Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp  
 290 295 300

Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro  
 305 310 315 320

Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly  
 325 330 335

Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu  
 340 345 350

Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala  
 355 360 365

Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu  
 370 375 380

Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser  
 385 390 395 400

Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu  
 405 410 415

Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly  
 420 425 430

Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys  
 435 440 445

Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser  
 450 455 460

Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 465 470 475

<210> 37

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggtacctcct ttgattagta ttttctatc ttaaagttac ttttatgtgg aggcattaac	60
atattgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg	180
gtggcacaac gtatttggca ttattagggt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcac tgcattcaat aaagaaaatt caatttcac catggcacca	360
ccagcatctc cgctgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat	540
ccgcatacgt acgaagacc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaaggt	660
atgttaaaaa catcatcagg taaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacacgc agttgatttt ttaggtgaag caggaattat gggatcaattt	780
agccatcata atattattcg ttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cgggtgctta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtggtt tacaattggt tggatgtta agaggaattg ctgcaggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa ataccctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagtat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaaact tagcagactt tgatcctcgt	1440
gtagtatctc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatgggttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc	1737

&lt;210&gt; 38

&lt;211&gt; 497

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 38

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
 50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln  
 65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu  
 85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val  
 100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys  
 115 120 125

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys  
 130 135 140

Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys  
 145 150 155 160

Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly  
 165 170 175

Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val  
 180 185 190

Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn  
 195 200 205

Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val  
 210 215 220

Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr  
 225 230 235 240

Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile  
 245 250 255

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser  
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly  
 275 280 285

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys  
 290 295 300

Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu  
 305 310 315 320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu  
 325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp  
 340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu  
 355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys  
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro  
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro  
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr  
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val  
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly



450

455

460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val  
 465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp  
 485 490 495

Leu

&lt;210&gt; 39

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion protein construct

&lt;400&gt; 39

```

ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac      60
atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata      120
atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg      180
gtggcacaacg gtatttggca ttattagggt aaaaaatgta gaaggagagt gaaacccatg      240
aaaaaaatta tgtagttttt tattacatta attttagtta gtttaccaat tgcacaacaa      300
acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca      360
ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc      420
gattataaag acgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc      480
ccagaagatg tgtatttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat      540
ccgcatacgt acgaagacc aaatcaagca gtattaaaat ttacaacaga aatacaccca      600
agttgtgtta caagacaaaa agttattgga gcagggtgaat tcggagaggt atataaaggt      660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca      720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggccaattt      780
agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt      840
attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatgggtgaa      900
tttagtgttt tacaattggg tggtatgtta agaggaattg ctgcaggtat gaaatattta      960
gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat     1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca     1080
acctatacaa catcggggagg taaaattcct attcgttgga cagcaccaga agctatcagt     1140

```

taccgtaa at ttacaagtgc atcagacgtg tggagttttg ggattgta at gtgggaagtt 1200  
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt 1260  
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg 1320  
atgcaatgtt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt 1380  
ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt 1440  
gtagtattc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc 1500  
gaatgggttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac 1560  
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaactgat tggagttaga 1620  
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat 1680  
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc 1737

<210> 40

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 40

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys  
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser  
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys  
50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln  
65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu  
85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val  
100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys

115	120	125
Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys 130	135	140
Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys 145	150	155 160
Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly 165	170	175
Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val 180	185	190
Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn 195	200	205
Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val 210	215	220
Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr 225	230	235 240
Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 245	250	255
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser 260	265	270
Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly 275	280	285
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys 290	295	300
Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu 305	310	315 320
Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu 325	330	335
Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp 340	345	350
Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu 355	360	365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys  
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro  
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro  
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr  
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val  
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly  
 450 455 460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val  
 465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp  
 485 490 495

Leu

<210> 41  
 <211> 1716  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 41  
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttgттаат gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240  
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300  
 aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360  
 ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420

```

aaacacagac gtagaaaaaa tcaacgtgct cgacaatccc cagaagatgt gtatttttcg      480
aaaagtgaac aattaaaacc attaaaaact tatgttgatc cgcatacgta cgaagaccca      540
aatcaagcag tattaaaatt tacaacagaa atacacccaa gttgtgttac aagacaaaaa      600
gttattggag caggtgaatt cggagaggta tataaaggta tgtaaaaac atcatcaggt      660
aaaaaagaag ttccgggtgc aattaaaacc ttaaaggcag gatatacaga aaaacagcga      720
gttgattttt taggtgaagc aggaattatg ggtcaattta gccatcataa tattattcgt      780
ttggaaggag taataagtaa atataaacca atgatgatta ttacagaata catggaaaac      840
ggtgcttttag ataaattttt acgtgaaaag gatgggtgaat ttagtgtttt acaattgggt      900
ggtatgttaa gaggaattgc tgcaggatg aaatatttag ctaatatgaa ttatgttcac      960
cgtgatttgg cagcaagaaa taccctagtc aattccaatt tagtatgtaa agttagtgat     1020
tttggtttta gcagagtatt agaagacgat ccagaggcaa cctatacaac atcgggaggt     1080
aaaattccta ttcgttggac agcaccagaa gctatcagtt accgtaaatt tacaagtgca     1140
tcagacgtgt ggagttttgg gattgtaatg tgggaagtta tgacatatgg agaaagacca     1200
tattgggaat taagtaatca tgaagttatg aaagcaatta acgatggatt tagattacca     1260
actccgatgg attgtccatc tgccatttat caactaatga tgcaatgttg gcaacaagaa     1320
agagcacgac gtccaaaatt tgcagatatt gttagtattt tagacaaatt aattcgtgca     1380
ccagatagtt taaaaacttt agcagacttt gatcctcgtg ttagtattcg attaccaagt     1440
acgtcagggt ccgaaggagt tccatttcgc acagtctccg aatgggttga atcaattaaa     1500
atgcaacaat acaccgaaca ctttatggca gcaggttaca cagcaatcga aaaagttggt     1560
caaatgacaa atgatgatat taaacgtatt ggagttagat taccaggcca ccagaaacgt     1620
attgcatatt ctttattagg tttaaaagat caagttaata ccgtgggaat tccaattgaa     1680
caaaaattaa tttccgaaga agacttataa gagctc                                1716

```

&lt;210&gt; 42

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Predicted fusion protein

&lt;400&gt; 42

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10          15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly

```

20	25	30
Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser		
35	40	45
Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys His Arg		
50	55	60
Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe		
65	70	75
Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His		
85	90	95
Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile		
100	105	110
His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe		
115	120	125
Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu		
130	135	140
Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln		
145	150	155
Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His		
165	170	175
His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met		
180	185	190
Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu		
195	200	205
Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu		
210	215	220
Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val		
225	230	235
His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val		
245	250	255
Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro		
260	265	270

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr  
 275 280 285

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val  
 290 295 300

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg  
 305 310 315 320

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp  
 325 330 335

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln  
 340 345 350

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe  
 355 360 365

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser  
 370 375 380

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro  
 385 390 395 400

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp  
 405 410 415

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala  
 420 425 430

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile  
 435 440 445

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr  
 450 455 460

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile  
 465 470 475 480

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
 485 490

<210> 43  
 <211> 9808  
 <212> DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion Protein Construct

&lt;400&gt; 43

```

ctttaaacgt ggatcatttt ctttaaattt atgctgacga ctttgaatt tgcctttttt      60
cttagcaatt tcgattcctt gtgcctgacg ttccttaatt ttttttcggt ctgattctgc    120
ttgatacttg tacaattcaa tgacaaggct attaatcaaa cgccttaaat tttcatcttc    180
aataccattc attgagggtg aatttaagac ttccagggtt gcccccttaa tttgaatttg    240
attcatcaat tctgttaatt ctttattatt tcgtcctaatt cgatctaatt cagtaacaat    300
aacaatatcc ccttcacgaa tatagttaag catagcttgt aattgtgggc gttcgaccga    360
ttgaccgctt aatttgtctg aaaagacctt agaaacgccc tgtaacgctt gtaattgccg    420
atctaagttc tgttctttgc tactgacacg tgcataacca attttagcca ttttcaacca    480
acctctaaaa ttctctcggg tgcaataacc aatcagcaat atctactttt tcaatttcaa    540
attgcttata agaaattgtc ttttcgtaag cgataaaatc ttgcgcatat tgttgctcat    600
taaaaatagc caccacttcg tcattttcta aaactcgata aataaatttt ttcattttac    660
tcctcctatt atgcccaact taaatgacct attcaccaag tcaattatac tgctaaaatc    720
atattaggac aaataggtat actctattga cctataaatg atagcaactt aaaagatcaa    780
gtgttcgctt cgctctcact gccctcgac gtttttagtag cctttccctc acttcgttca    840
gtccaagcca actaaaagtt ttcgggctac tctctccttc tccccctaatt aattaattaa    900
aatcttactc tgtatatttc tgctaatacat tcactaaaca gcaaagaaaa acaaacacgt    960
atcatagata taaatgtaat ggcatagtgc gggttttatt ttcagcctgt atcgtagcta   1020
aacaaatcga gttgtgggtc cgttttgggg cgttctgcc aattgttttag agtttcttga   1080
ataaatgtac gttctaaatt aaacgaagct gtcagcgcct ttatatagct ttctcgttct   1140
tcttttttta atttaatgat cgatagcaac aatgatttaa cactagcaag ttgaatgcc a   1200
ccatttcttc ctggtttaat cttaaagaaa atttctgat tcgccttcag taccttcagc   1260
aatttatcta atgtccgttc aggaatgcct agcacttctc taatctcttt tttggtcgtc   1320
gctaaataag gcttgtatac atcgcttttt tcgctaatat aagccattaa atcttctttc   1380
cattctgaca aatgaacacg ttgacgttcg cttctttttt tcttgaattt aaaccacctt   1440
tgacggacaa ataaatcttt actgggttaa tcacttgata cccaagcttt gcaaagaatg   1500
gtaatgtatt ccctattagc cccttgatag ttttctgaat aggcacttct aacaattttg   1560
attacttctt tttcttctaa gggttgatct aatcgattat taaactcaaa catattatat   1620
tcgcacgttt cgattgaata gcctgaacta aagtaggcta aagagagggt aaacataacg   1680

```



ctattgcgcc ctactaaacc cttttctcct gaaaatttcg tttcgtgcaa taagagatta	1740
aaccagggtt catctacttg ttttttgcc tctgtaccgc ttaaaaccgt tagacttgaa	1800
cgagtaaagc ccttattatc tgtttgtttg aaagaccaat cttgccattc tttgaaagaa	1860
taacggtaat tgggatcaaa aaattctaca ttgtccgttc ttggtatacg agcaatccca	1920
aatgattgc acgtagatc aactggcaaa gactttccaa aatattctcg gatattttgc	1980
gagattatth tggctgcttt gacagattta aattctgatt ttgaagtcac atagactggc	2040
gtttctaaaa caaaatatgc ttgataacct ttatcagatt tgataattaa cgtaggcata	2100
aaacctaaat caatagctgt tgttaaaata tcgcttgctg aaatagtttc tttttccgtg	2160
tgaatatcaa aatcaataaa gaaggatttg atttgtctta aattgttttc agaatgtcct	2220
ttagtgatg aacggttttc gtctgcatac gtaccataac gataaacgtt tgggtgtccaa	2280
tgcgtaaagc tatcttgatt ttcgtgaac gcttcttcgg aagtcagaac aacgccacgt	2340
ccgccaatca tgcctttttt tgagcgatac gcaaaaatag cccctttact tttacctggc	2400
ttggtagtga ttgagcgaat tttactatth ttaaatttgt actttaacaa gccgtcatga	2460
agcacagttt ctacaacaaa agggatattc attcagctgt tctcctttct tacgaaaatt	2520
aattagttag aagctacgat caaagttgaa tcacaacaaa aaaggcaatc aactaagttt	2580
ttcttaattg attgcctggt atcttcttaa agacttgaaa tccctcaaa aaccgatat	2640
aatgggttta cagatattta agtatctgat taataaagta attaaatact ttaccaaatt	2700
ttgggtctcg acttctttaa ttgattgggt gtaatcaatt aaggctcgca gttaaaattt	2760
ctcaggcttt aactggctcg ggctcttttt ttgtattctt tattcagttc gttgtttcgt	2820
tatatctagt atatcgcttt ttaaaaaaat aagcaatgat ttcgtgcatt attcacacga	2880
aatcattgct tttttcttct tccatttcta actccaatgt tacttgttct gtttctgggt	2940
ctggttctgt tggctcattt gggattaaat ccactactag cgttgagtta gttccgtctc	3000
taatagccgg ttaagtaata gccggttaag tgggtcaaact ttgggaaaat ctcaaccgcg	3060
attaagtttt gatgccatga caatcgttgg aaatttgaac aaaactaatg ctaaaaagct	3120
atctgacttt atgagtgtag agccacaaat acgactttgg gatatacttc aaacaaagtt	3180
taaagctaag gcacttcaag aaaaagttha tatcgaatat gacaaagtaa aagcagatac	3240
ttgggataga cgtaatatgc gtgttgaaat taatcccaat aaactcacac atgaagaaat	3300
gatttggtta aaacaaaata ttatcgacta catggaagat gacggtttta caagattaga	3360
cttagctttt gattttgaag atgatttgag cgattactat gcaatgactg ataaagcagt	3420
taagaaaact gttttttatg gtcgtaatgg caagccagaa acaaaatatt ttgggtgtccg	3480

tgatagtgat agattttatta gaattttataa taaaaaaciaa gaacgtaaag ataacgcaga	3540
tgttgaagtt gtgtttgaac atttatggcg tgtagaagtt gaattaaaaa gagatatggt	3600
tgattactgg aatgattggt ttaatgattt acacatcttt gaaacctgcg tgggctactt	3660
tagaaaaaat taatgagcaa gctatggttt atactttgtt gcatgaagaa agtatgtggg	3720
gaaagctaag taagaatact aagactaaat ttaaaaaaatt gattagagaa atatctccaa	3780
ttgatttaac ggaattaatg aaatcgactt taaaagcgaa cgaaaaaciaa ttgcaaaagc	3840
agattgattt ttggcaacgt gaatttaggt tttggaagta aaataagttt tatttgataa	3900
aaattgctaa ttcagtataa ttaatattta cgagggtgaca taacgtatga aaaaatcaga	3960
ggattattcc tcctaaatat aaaaatttaa aatttaggag gaagttatat atgactttta	4020
atattattga attagaaaaat tgggtagaaa aagaatattt tgaacactat tttaatcagc	4080
aaactactta tagcattact aaagaaattg atattacttt gtttaaagat atgataaaaa	4140
agaaaggata tgaaatttat ccctctttta tttatgcaat tatggaagtt gtaaataaaa	4200
ataaagtgtt tagaacagga attaatagtg agaataaatt aggttatttg gataagttaa	4260
atcctttgta tacagttttt aataagcaaa ctgaaaaaatt tactaacatt tggactgaat	4320
ctgataaaaa cttcatttct ttttataata attataaaaa tgacttgctt gaataaaag	4380
ataaagaaga aatgtttcct aaaaaaccga tacctgaaaa caccataccg atttcaatga	4440
ttccttggtat tgatttttagt tcattttaatt taaatatttg taacaatagc agctttttat	4500
tgctattat tacgataggt aaattttata gtgagaataa taaaatttat ataccagttg	4560
ctctgcaact tcatcattct gtatgtgatg gttaccatgc ttcactattt atgaatgaat	4620
ttcaagatat aattcatagg gtagatgatt ggatttagtt tttagatttt gaaagtgaat	4680
ttaattttat acacgtaagt gatcataaaa tttatgaacg tataacaacc acattttttg	4740
gttgcttggt gttttgattt tgaatttggt tttgaactta tggactgatt tattcagtc	4800
attttttggt cttgcacaaa aactagcctc gcagagcaca cgcattaatg acttatgaaa	4860
cgtagtaaat aagtctagtg tgttatactt tacttggaag atgcaccgaa taaaaaatat	4920
tgaagaacia ctagcaaaag attttaaaga gttattttat ttttaagtct tataacatga	4980
gtgaagcgaa tttttaaatt tcgatagaaa tttttacatc aaaaagcccc ctgtcaaaat	5040
tgacgaaggg ggttttttgg cgcacgcttt tcgttagaaa tatacaagat tgaaaatcgt	5100
gtataagtgc gccctttggt ttgaacttag cacgttacat caatttttta aaatgatgta	5160
taagtgcgcc cttttaaatt ttgagtgatt atattttttg agttagaaaa agggattggg	5220
aaaatttccc aaaataattt aaaaaataag caaaaatttt cgatagagaa tgtgctattt	5280
tttgtcaaag gtgtatacct tgactgtgct tgctgttaca ttaagtttat ttttaagtta	5340

ttaaaaaaga aatagctttt aaagtttggc tcgctgtcgc tttataaagc tgattgactt	5400
ttgattgcaa actacttaaa gaaaacaaac tcggactatt cgttttcttc tctttggttt	5460
gaacatcagc aattatcccc tcttgattgc ctatttttagc ttgttttagaa gaaacaaaag	5520
ctaaaagctc ctcttggggtt ttaaaacgct gtgtgggggct tagaacgccc ttaaacgacc	5580
cttggttttac ttttatacta gcttccacct cgaaaaaagg ttcttttttta aaattctcta	5640
tggcttcctg gcgctgaaaa aataagggtat aagggtgggcg tttgaacacg tcctagttaa	5700
aatgtacctt gtacgccccct tctgttgtaa atttaacgta tacaaagggc ttgcgttcat	5760
gccgatcaac caatcggcaa tttggcgtgt ttgcgcttct tgataaaagg gatagtaatt	5820
cattccaggt tgcaaatttt gaaaaccgct tcggattaca tctttttcta agctattgat	5880
ccatagtctt ttaaattgtt tatcttttga aaaggcattt gctttatgga taatcgacca	5940
ggcgatattt tcaccttctc tgctcgtatc tgttgcaaca ataattgtat ttgccttttt	6000
gagaagttct gcaacaattt taaactgctt tcccttatct tttgcaactt caaaatcgta	6060
tcgatcagga aaaatcggca aagattcaag tttccaattt tgccactttt cgtcataatg	6120
acctggttct gctaattcca ctaaattgcc aaaaccaaag gtgataaacg tttcatctgt	6180
aaatagtggg tctttgatct caaaataacc gtcttttttg gtgctttgtt ttaaagcact	6240
tgcgtaggct aatgcctggc ttggtttttc agctaaaata accgtactca ttaactatcc	6300
ctcttttcat tgttttttct ttgatcgact gtcacgttat atcttgctcg ataccttcta	6360
aacgttcggc gattgattcc agtttgttct tcaacttctt tatcggataa accattcaaa	6420
aacaaatcga aagcatggat gcgcgcgctg cggctgctgg agatggcgga cgcgatggat	6480
atgttctgcc aagggttggg ttgcgcattc acagttctcc gcaagaattg attggctcca	6540
attcttggag tggatgaatc gttagcgagg tgccgccggc ttccattcag gtcgaggtgg	6600
cccggctcca tgcaccgga cgcaacggcg ggaggcagac aaggtatagg gcggcgcccta	6660
caatccatgc caaccgctc catgtgctcg ccgaggcggc ataaatcgcc gtgacgatca	6720
gcggtccagt gatcgaagtt aggctggtaa gagccgcgag cgatccttga agctgtccct	6780
gatggtcgtc atctacctgc ctggacagca tggcctgcaa cgcgggcac cccgatgccgc	6840
cggaagcgag aagaatcata atggggaagg ccatccagcc tcgctgcgca atacgactca	6900
ctatagggcg aattgggtac cgggcccccc ctcgaggtcg acggtatcga taagcttgat	6960
atcgaattcc tgcagcccg gggatccact agttctagag cggccgccac cgcggtggag	7020
ctccagcttt tgttcccttt agtgagggtt aatgctagaa atattttatc tgattaataa	7080
gatgatcttc ttgagatcgt tttggtctgc gcgtaatctc ttgctctgaa aacgaaaaaa	7140

ccgccttgca	gggcgggtttt	tccaaggttc	tctgagctac	caactctttg	aaccgaggta	7200
actggcttgg	aggagcgcag	tcaccaaaac	ttgtcctttc	agtttagcct	taaccggcgc	7260
atgacttcaa	gactaactcc	tctaaatcaa	ttaccagtgg	ctgctgccag	tggtgctttt	7320
gcatgtcttt	cggggttggg	ctcaagacga	tagttaccgg	ataaggcgca	gcggtcggac	7380
tgaacggggg	gttcgtgcat	acagtccagc	ttggagcgaa	ctgcctaccc	ggaactgagt	7440
gtcaggcgtg	gaatgagaca	aacgcggcca	taacagcgga	atgacaccgg	taaaccgaaa	7500
ggcaggaaca	ggagagcgca	cgaggggagc	gccaggggga	aacgcctggg	atctttatag	7560
tcctgtcggg	tttcgccacc	actgatttga	gcgtcagatt	tcgtgatgct	tgtcaggggg	7620
gcggagccta	tggaaaaacg	gctttgccgc	ggccctctca	cttcctgttt	aagtatcttc	7680
ctggcatctt	ccaggaaaac	tccgccccgt	tcgtaagcca	tttcgctcgc	ccgcagtcga	7740
acgaccgagc	gtagcgagtc	agtgagcgag	gaagcggaat	atatcctgta	tcacatatcc	7800
tgctgacgca	ccggtgcagc	cttttttctc	ctgccacatg	aagcacttca	ctgacaccct	7860
catcagtgcc	aacatagtaa	gccagtatac	actccgctag	cgctgatgtc	cggcgggtgt	7920
tttgccgtta	cgcaccaccc	cgtcagtagc	tgaacaggag	ggacagctga	tagaaacaga	7980
agccactgga	gcacctcaaa	aacaccatca	tacactaaat	cagtaagttg	gcagcatcac	8040
ccgacgcact	ttgcgccgaa	taaataacct	tgacggaaga	tcacttcgca	gaataaataa	8100
atcctgggtg	ccctgttgat	accgggaagc	cctgggcca	cttttggcga	aaatgagacg	8160
ttgatcggca	cgtaagaggt	tccaactttc	accataatga	aataagatca	ctaccgggcg	8220
tattttttga	gttatcgaga	ttttcaggag	ctaaggaagc	taaaatggag	aaaaaatca	8280
ctggatatac	caccgttgat	atatcccaat	ggcatcgtaa	agaacatttt	gaggcatttc	8340
agtcagttgc	tcaatgtacc	tataaccaga	ccgttcagct	ggatattacg	gcctttttta	8400
agaccgtaaa	gaaaaataag	cacaagtttt	atccggcctt	tattcacatt	cttgcgccgc	8460
tgatgaatgc	tcacccggaa	ttccgtatgg	caatgaaaga	cgggtgagctg	gtgatatggg	8520
atagtgttca	cccttggtac	accgttttcc	atgagcaaac	tgaaacgttt	tcacgcgtct	8580
ggagtgaata	ccacgacgat	ttccggcagt	ttctacacat	atattcgcaa	gatgtggcgt	8640
gttacggtga	aaacctggcc	tatttcctta	aagggtttat	tgagaatatg	tttttcgtct	8700
cagccaatcc	ctgggtgagt	ttcaccagtt	ttgatttaaa	cgtggccaat	atggacaact	8760
tcttcgcccc	cgttttcacc	atgggcaaat	attatacgca	aggcgacaag	gtgctgatgc	8820
cgctggcgat	tcaggttcat	catgccgtct	gtgatggctt	ccatgtcggc	agaatgctta	8880
atgaattaca	acagtactgc	gatgagtggc	agggcggggc	gtaatttttt	taaggcagtt	8940
attggtgccc	ttaaaccgct	ggtgctacgc	ctgaataagt	gataataagc	ggatgaatgg	9000

cagaaattcg aaagcaaatt cgacccgggtc gtcgggttcag ggcaggggtcg ttaaataagcc 9060  
 gcttatgtct attgctgggt taccgggttta ttgactaccg gaagcagtgt gaccgtgtgc 9120  
 ttctcaaatg cctgaggcca gtttgtctcag gctctccccg tggaggtaat aattgacgat 9180  
 atgatcattt attctgcctc ccagagcctg ataaaaacgg ttagcgcttc gttaatacag 9240  
 atgtagggtg tccacagggg agccagcagc atcctgcgat gcagatccgg aacataatgg 9300  
 tgcagggcgc ttgtttcggc gtgggtatgg tggcaggccc cgtggccggg ggactgttgg 9360  
 gcgctgccgg cacctgtcct acgagttgca tgataaagaa gacagtcata agtgccggcg 9420  
 cgatagtcac gccccgcgcc caccggaagg agctaccgga cagcgggtgcg gactgttgta 9480  
 actcagaata agaaatgagg ccgctcatgg cgttgactct cagtcatagt atcgtgggtat 9540  
 caccgggttg ttccactctc tgttgcgggc aacttcagca gcacgtaggg gacttccgcg 9600  
 tttccagact ttacgaaaca cggaaccga agaccattca tgttgttgct caggtcgcag 9660  
 acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca ttctgctaac 9720  
 cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg atcatgcgca 9780  
 cccgtggcca ggaccaacg ctgcccga 9808

<210> 44  
 <211> 26  
 <212> PRT  
 <213> *Listeria monocytogenes*

<400> 44

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu  
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp  
 20 25

<210> 45  
 <211> 59  
 <212> PRT  
 <213> *Listeria monocytogenes*

<400> 45

Met Thr Asp Lys Lys Ser Glu Asn Gln Thr Glu Lys Thr Glu Thr Lys  
 1 5 10 15

Glu Asn Lys Gly Met Thr Arg Arg Glu Met Leu Lys Leu Ser Ala Val  
 20 25 30

Ala Gly Thr Gly Ile Ala Val Gly Ala Thr Gly Leu Gly Thr Ile Leu

35

40

45

Asn Val Val Asp Gln Val Asp Lys Ala Leu Thr  
 50 55

<210> 46  
 <211> 53  
 <212> PRT  
 <213> Bacillus subtilus

<400> 46

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu  
 1 5 10 15

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly  
 20 25 30

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser  
 35 40 45

Val Gly Ala Phe Gly  
 50

<210> 47  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 47

gtcaaaacat acgctcttat c

21

<210> 48  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 48

acataatcag tccaaagtag atgc

24

<210> 49  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 49  
ctctggtacc tcctttgatt agtatattc 29

<210> 50  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 50  
ctctggatcc atccgcgtgt ttcttttcg 29

<210> 51  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Epitope insert

<400> 51  
gattataaaag atgatgatga taaa 24

<210> 52  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Epitope

<400> 52

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 53  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Epitope insert

<400> 53  
gaacaaaaat taattagtga agaagattta 30

<210> 54  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 54

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
1 5 10

<210> 55

<211> 9

<212> PRT

<213> Mus sp.

<400> 55

Ser Pro Ser Tyr Val Tyr His Gln Phe  
1 5

<210> 56

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Epitope

<400> 56

Ser Pro Ser Tyr Ala Tyr His Gln Phe  
1 5

<210> 57

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 57

ctctggtacc tcctttgatt agtatattc

29

<210> 58

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 58

caatggatcc ctcgagatca taatttactt catccc

36

<210> 59

<211> 32

<212> DNA



## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 59

atttctcgag tccatggggg gttctcatca tc

32

&lt;210&gt; 60

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 60

ggtgctcgag tgcggccgca agctt

25

&lt;210&gt; 61

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 61

cgattcccct agttatgttt accaccaatt tgctgca

37

&lt;210&gt; 62

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 62

gcaaattggt ggtaaacata actaggggaa t

31

&lt;210&gt; 63

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Epitope insert

&lt;400&gt; 63

agtcgaagtt atgcatatca tcaattt

27

&lt;210&gt; 64

&lt;211&gt; 33

&lt;212&gt; DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 64

cgatagtcga agttatgcat atcatcaatt tgc

33

&lt;210&gt; 65

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 65

gtcgcaaatt gatgatatgc ataacttgga ctat

34

&lt;210&gt; 66

&lt;211&gt; 8

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Consensus Sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1)

&lt;223&gt; n is a, c, g, or u

&lt;400&gt; 66

naggaggu

8

&lt;210&gt; 67

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Listeria monocytogenes

&lt;400&gt; 67

aaggagagt aaacccatg

19

&lt;210&gt; 68

&lt;211&gt; 240

&lt;212&gt; DNA

&lt;213&gt; Listeria monocytogenes

&lt;400&gt; 68

ggtacctcct ttgattagta tttcctatc ttaaagtgac ttttatgttg aggcattaac

60

atattgttaac gacgataaag ggacagcagg actagaataa agctataaag caagcatata

120

atattgcgtt tcattcttag aagcgaattt cgccaatatt ataattatca aaagagaggg

180

gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg

240

<210> 69  
 <211> 240  
 <212> DNA  
 <213> *Listeria monocytogenes*

<400> 69  
 ggtacctcct ttgattagta tttcctatc ttaaagttac ttttatgtgg aggcattaac 60  
 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120  
 atattgcggtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180  
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240

<210> 70  
 <211> 5  
 <212> PRT  
 <213> *Listeria monocytogenes*

<400> 70

Thr Glu Ala Lys Asp  
 1 5

<210> 71  
 <211> 5  
 <212> PRT  
 <213> *Listeria monocytogenes*

<400> 71

Asp Lys Ala Leu Thr  
 1 5

<210> 72  
 <211> 5  
 <212> PRT  
 <213> *Bacillus subtilus*

<400> 72

Val Gly Ala Phe Gly  
 1 5